

# TRhizo-urbanMicrobiome

## Effect Size Calculations

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## Load Packages & Data

# Alpha Diversity Effect Sizes

## ASV Richness

### Distance

```
## Get model residuals
ASV.richness.by.distance.residual.df <- df.residual(
  ASV.richness.by.distance.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
ASV.richness.by.distance.compartment.eta.squared <- F_to_eta2(
  652.9, 1, ASV.richness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
ASV.richness.by.distance.root.eta.squared <- F_to_eta2(
  0.087, 0.411, ASV.richness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
ASV.richness.by.distance.soil.eta.squared <- F_to_eta2(
  2.848, 2.939, ASV.richness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
ASV.richness.by.distance.population.eta.squared <- F_to_eta2(
  0.292, 7.687, ASV.richness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
ASV.richness.by.distance.effect.sizes <- tibble(
  Compartment = ASV.richness.by.distance.compartment.eta.squared,
  Smooth_by_Root = ASV.richness.by.distance.root.eta.squared,
  Smooth_by_Soil = ASV.richness.by.distance.soil.eta.squared,
  Population = ASV.richness.by.distance.population.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
ASV.richness.by.HII.residual.df <- df.residual(
  ASV.richness.by.HII.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
ASV.richness.by.HII.compartment.eta.squared <- F_to_eta2(
  637.2, 1, ASV.richness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
ASV.richness.by.HII.root.HII.eta.squared <- F_to_eta2(
  0.138, 0.505, ASV.richness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
ASV.richness.by.HII.soil.HII.eta.squared <- F_to_eta2(
  1.336, 0.896, ASV.richness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
ASV.richness.by.HII.population.eta.squared <- F_to_eta2(
  0.411, 9.908, ASV.richness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
ASV.richness.by.ISC.effect.sizes <- tibble(
  Compartment = ASV.richness.by.HII.compartment.eta.squared,
  Smooth_by_Root = ASV.richness.by.HII.root.HII.eta.squared,
  Smooth_by_Soil = ASV.richness.by.HII.soil.HII.eta.squared,
  Population = ASV.richness.by.HII.population.eta.squared
)
```



## Mean ISC

```
## Get model residuals
ASV.richness.by.ISC.residual.df <- df.residual(
  ASV.richness.by.ISC.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
ASV.richness.by.ISC.compartment.eta.squared <- F_to_eta2(
  665.2, 1, ASV.richness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
ASV.richness.by.ISC.root.ISC.eta.squared <- F_to_eta2(
  0.135, 0.551, ASV.richness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
ASV.richness.by.ISC.soil.ISC.eta.squared <- F_to_eta2(
  4.582, 5.933, ASV.richness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
ASV.richness.by.ISC.population.eta.squared <- F_to_eta2(
  0.003, 0.092, ASV.richness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
ASV.richness.by.HII.effect.sizes <- tibble(
  Compartment = ASV.richness.by.ISC.compartment.eta.squared,
  Smooth_by_Root = ASV.richness.by.ISC.root.ISC.eta.squared,
  Smooth_by_Soil = ASV.richness.by.ISC.soil.ISC.eta.squared,
  Population = ASV.richness.by.ISC.population.eta.squared
)
```

## ASV Richness Effect Size Summary

Table 1: Summary of effect sizes (partial eta-squared) for the ASV richness GAMMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil	Population
Distance	0.67180	0.00011	0.02557	0.00699
HII	0.67285	0.00023	0.07754	0.00000
ISC	0.66660	0.00022	0.00374	0.01262

## Inverse Simpson

### Distance

```
## Get model residuals
inverse.simpson.by.distance.residual.df <- df.residual(
  inverse.simpson.by.distance.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
inverse.simpson.by.distance.compartment.eta.squared <- F_to_eta2(
  1331, 1, inverse.simpson.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
inverse.simpson.by.distance.root.eta.squared <- F_to_eta2(
  0.0001, 0.002, inverse.simpson.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
inverse.simpson.by.distance.soil.eta.squared <- F_to_eta2(
  10.988, 4.038, inverse.simpson.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
inverse.simpson.by.distance.population.eta.squared <- F_to_eta2(
  3.694, 26.605, inverse.simpson.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
inverse.simpson.by.distance.effect.sizes <- tibble(
  Compartment = inverse.simpson.by.distance.compartment.eta.squared,
  Smooth_by_Root = inverse.simpson.by.distance.root.eta.squared,
  Smooth_by_Soil = inverse.simpson.by.distance.soil.eta.squared,
  Population = inverse.simpson.by.distance.population.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
inverse.simpson.by.HII.residual.df <- df.residual(
  inverse.simpson.by.HII.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
inverse.simpson.by.HII.compartment.eta.squared <- F_to_eta2(
  1347, 1, inverse.simpson.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
inverse.simpson.by.HII.root.HII.eta.squared <- F_to_eta2(
  0.00001, 0.001, inverse.simpson.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
inverse.simpson.by.HII.soil.HII.eta.squared <- F_to_eta2(
  14.595, 4.233, inverse.simpson.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
inverse.simpson.by.HII.population.eta.squared <- F_to_eta2(
  2.925, 25.114, inverse.simpson.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
inverse.simpson.by.ISC.effect.sizes <- tibble(
  Compartment = inverse.simpson.by.HII.compartment.eta.squared,
  Smooth_by_Root = inverse.simpson.by.HII.root.HII.eta.squared,
  Smooth_by_Soil = inverse.simpson.by.HII.soil.HII.eta.squared,
  Population = inverse.simpson.by.HII.population.eta.squared
)
```

## Mean ISC

```
## Get model residuals
inverse.simpson.by.ISC.residual.df <- df.residual(
  inverse.simpson.by.ISC.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
inverse.simpson.by.ISC.compartment.eta.squared <- F_to_eta2(
  1324, 1, inverse.simpson.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
inverse.simpson.by.ISC.root.ISC.eta.squared <- F_to_eta2(
  0.00001, 0.002, inverse.simpson.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
inverse.simpson.by.ISC.soil.ISC.eta.squared <- F_to_eta2(
  10.431, 4.372, inverse.simpson.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
inverse.simpson.by.ISC.population.eta.squared <- F_to_eta2(
  3.523, 26.064, inverse.simpson.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
inverse.simpson.by.HII.effect.sizes <- tibble(
  Compartment = inverse.simpson.by.ISC.compartment.eta.squared,
  Smooth_by_Root = inverse.simpson.by.ISC.root.ISC.eta.squared,
  Smooth_by_Soil = inverse.simpson.by.ISC.soil.ISC.eta.squared,
  Population = inverse.simpson.by.ISC.population.eta.squared
)
```

## Inverse Simpson Effect Size Summary

Table 2: Summary of effect sizes (partial eta-squared) for the inverse Simpson GAMMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil	Population
Distance	0.81639	0	0.12908	0.24716
HII	0.81549	0	0.13212	0.23461
ISC	0.81753	0	0.17046	0.19636

## ASV Evenness

### Distance

```
## Get model residuals
ASV.evenness.by.distance.residual.df <- df.residual(
  ASV.evenness.by.distance.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
ASV.evenness.by.distance.compartment.eta.squared <- F_to_eta2(
  476.1, 1, ASV.evenness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
ASV.evenness.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, ASV.evenness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
ASV.evenness.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, ASV.evenness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
ASV.evenness.by.distance.population.eta.squared <- F_to_eta2(
  2.787, 25.038, ASV.evenness.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
ASV.evenness.by.distance.effect.sizes <- tibble(
  Compartment = ASV.evenness.by.distance.compartment.eta.squared,
  Smooth_by_Root = ASV.evenness.by.distance.root.eta.squared,
  Smooth_by_Soil = ASV.evenness.by.distance.soil.eta.squared,
  Population = ASV.evenness.by.distance.population.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
ASV.evenness.by.HII.residual.df <- df.residual(
  ASV.evenness.by.HII.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
ASV.evenness.by.HII.compartment.eta.squared <- F_to_eta2(
  637.2, 1, ASV.evenness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
ASV.evenness.by.HII.root.HII.eta.squared <- F_to_eta2(
  0.006, 0.043, ASV.evenness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
ASV.evenness.by.HII.soil.HII.eta.squared <- F_to_eta2(
  0.00001, 0.001, ASV.evenness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
ASV.evenness.by.HII.population.eta.squared <- F_to_eta2(
  2.786, 25.031, ASV.evenness.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
ASV.evenness.by.ISC.effect.sizes <- tibble(
  Compartment = ASV.evenness.by.HII.compartment.eta.squared,
  Smooth_by_Root = ASV.evenness.by.HII.root.HII.eta.squared,
  Smooth_by_Soil = ASV.evenness.by.HII.soil.HII.eta.squared,
  Population = ASV.evenness.by.HII.population.eta.squared
)
```



## Mean ISC

```
## Get model residuals
ASV.evenness.by.ISC.residual.df <- df.residual(
  ASV.evenness.by.ISC.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
ASV.evenness.by.ISC.compartment.eta.squared <- F_to_eta2(
  476.5, 1, ASV.evenness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
ASV.evenness.by.ISC.root.ISC.eta.squared <- F_to_eta2(
  0.00001, 0.00001, ASV.evenness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
ASV.evenness.by.ISC.soil.ISC.eta.squared <- F_to_eta2(
  0.173, 0.414, ASV.evenness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
ASV.evenness.by.ISC.population.eta.squared <- F_to_eta2(
  2.737, 24.884, ASV.evenness.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
ASV.evenness.by.HII.effect.sizes <- tibble(
  Compartment = ASV.evenness.by.ISC.compartment.eta.squared,
  Smooth_by_Root = ASV.evenness.by.ISC.root.ISC.eta.squared,
  Smooth_by_Soil = ASV.evenness.by.ISC.soil.ISC.eta.squared,
  Population = ASV.evenness.by.ISC.population.eta.squared
)
```

### ASV Evenness Effect Size Summary

Table 3: Summary of effect sizes (partial eta-squared) for the ASV evenness GAMMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil	Population
Distance	0.60955	0	0.00000	0.18621
HII	0.60996	0	0.00024	0.18269
ISC	0.67634	0	0.00000	0.18613

## Faith's PD

### Distance

```
## Get model residuals
faiths.PD.by.distance.residual.df <- df.residual(
  faiths.PD.by.distance.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
faiths.PD.by.distance.compartment.eta.squared <- F_to_eta2(
  809.2, 1, faiths.PD.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
faiths.PD.by.distance.root.eta.squared <- F_to_eta2(
  0.151, 0.533, faiths.PD.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
faiths.PD.by.distance.soil.eta.squared <- F_to_eta2(
  4.837, 3.636, faiths.PD.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
faiths.PD.by.distance.population.eta.squared <- F_to_eta2(
  0.374, 9.280, faiths.PD.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
faiths.PD.by.distance.effect.sizes <- tibble(
  Compartment = faiths.PD.by.distance.compartment.eta.squared,
  Smooth_by_Root = faiths.PD.by.distance.root.eta.squared,
  Smooth_by_Soil = faiths.PD.by.distance.soil.eta.squared,
  Population = faiths.PD.by.distance.population.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
faiths.PD.by.HII.residual.df <- df.residual(
  faiths.PD.by.HII.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
faiths.PD.by.HII.compartment.eta.squared <- F_to_eta2(
  809.2, 1, faiths.PD.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
faiths.PD.by.HII.root.HII.eta.squared <- F_to_eta2(
  0.332, 0.678, faiths.PD.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
faiths.PD.by.HII.soil.HII.eta.squared <- F_to_eta2(
  2.258, 0.927, faiths.PD.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
faiths.PD.by.HII.population.eta.squared <- F_to_eta2(
  0.593, 12.636, faiths.PD.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
faiths.PD.by.ISC.effect.sizes <- tibble(
  Compartment = faiths.PD.by.HII.compartment.eta.squared,
  Smooth_by_Root = faiths.PD.by.HII.root.HII.eta.squared,
  Smooth_by_Soil = faiths.PD.by.HII.soil.HII.eta.squared,
  Population = faiths.PD.by.HII.population.eta.squared
)
```

## Mean ISC

```
## Get model residuals
faiths.PD.by.ISC.residual.df <- df.residual(
  faiths.PD.by.ISC.GAMM
)

## Calculate effect sizes
# Compartment (parametric)
faiths.PD.by.ISC.compartment.eta.squared <- F_to_eta2(
  856.4, 1, faiths.PD.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
faiths.PD.by.ISC.root.ISC.eta.squared <- F_to_eta2(
  0.230, 0.678, faiths.PD.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
faiths.PD.by.ISC.soil.ISC.eta.squared <- F_to_eta2(
  6.677, 6.443, faiths.PD.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of population random effect
faiths.PD.by.ISC.population.eta.squared <- F_to_eta2(
  0.035, 1.149, faiths.PD.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
faiths.PD.by.HII.effect.sizes <- tibble(
  Compartment = faiths.PD.by.ISC.compartment.eta.squared,
  Smooth_by_Root = faiths.PD.by.ISC.root.ISC.eta.squared,
  Smooth_by_Soil = faiths.PD.by.ISC.soil.ISC.eta.squared,
  Population = faiths.PD.by.ISC.population.eta.squared
)
```

## Faiths PD Effect Size Summary

Table 4: Summary of effect sizes (partial eta-squared) for the ASV richness GAMMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil	Population
Distance	0.71881	0.00025	0.05263	0.01085
HII	0.72691	0.00048	0.11794	0.00012
ISC	0.71932	0.00071	0.00659	0.02318

# Beta Diversity Effect Sizes

## Bray-Curtis Distance

### Distance

```
## Get model residuals
BC.multivariate.dispersion.by.distance.residual.df <- df.residual(
  BC.multivariate.dispersion.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
BC.dispersion.by.distance.compartment.eta.squared <- F_to_eta2(
  109.6, 1, BC.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
BC.dispersion.by.distance.root.eta.squared <- F_to_eta2(
  1.002, 2.226, BC.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
BC.dispersion.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, BC.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
BC.dispersion.by.distance.effect.sizes <- tibble(
  Compartment = BC.dispersion.by.distance.compartment.eta.squared,
  Smooth_by_Root = BC.dispersion.by.distance.root.eta.squared,
  Smooth_by_Soil = BC.dispersion.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
BC.multivariate.dispersion.by.HII.residual.df <- df.residual(
  BC.multivariate.dispersion.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
BC.dispersion.by.HII.compartment.eta.squared <- F_to_eta2(
  96.9, 1, BC.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
BC.dispersion.by.HII.root.eta.squared <- F_to_eta2(
  0.016, 0.127, BC.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
BC.dispersion.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, BC.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
BC.dispersion.by.HII.effect.sizes <- tibble(
  Compartment = BC.dispersion.by.HII.compartment.eta.squared,
  Smooth_by_Root = BC.dispersion.by.HII.root.eta.squared,
  Smooth_by_Soil = BC.dispersion.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
BC.multivariate.dispersion.by.ISC.residual.df <- df.residual(
  BC.multivariate.dispersion.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
BC.dispersion.by.ISC.compartment.eta.squared <- F_to_eta2(
  96.7, 1, BC.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
BC.dispersion.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, BC.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
BC.dispersion.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, BC.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
BC.dispersion.by.ISC.effect.sizes <- tibble(
  Compartment = BC.dispersion.by.ISC.compartment.eta.squared,
  Smooth_by_Root = BC.dispersion.by.ISC.root.eta.squared,
  Smooth_by_Soil = BC.dispersion.by.ISC.soil.eta.squared
)
```

## Bray-Curtis Multivariate Dispersion Effect Size Summary

Table 5: Summary of effect sizes (partial eta-squared) for the Bray-Curtis multivariate dispersion GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.62495	0.03280	0
HII	0.58808	0.00003	0
ISC	0.58713	0.00000	0

## UniFrac Distance

### Distance

```
## Get model residuals
UniFrac.multivariate.dispersion.by.distance.residual.df <- df.residual(
  UniFrac.multivariate.dispersion.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
UniFrac.dispersion.by.distance.compartment.eta.squared <- F_to_eta2(
  68.4, 1, UniFrac.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
UniFrac.dispersion.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, UniFrac.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
UniFrac.dispersion.by.distance.soil.eta.squared <- F_to_eta2(
  0.001, 0.012, UniFrac.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
UniFrac.dispersion.by.distance.effect.sizes <- tibble(
  Compartment = UniFrac.dispersion.by.distance.compartment.eta.squared,
  Smooth_by_Root = UniFrac.dispersion.by.distance.root.eta.squared,
  Smooth_by_Soil = UniFrac.dispersion.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
UniFrac.multivariate.dispersion.by.HII.residual.df <- df.residual(
  UniFrac.multivariate.dispersion.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
UniFrac.dispersion.by.HII.compartment.eta.squared <- F_to_eta2(
  71.7, 1, UniFrac.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
UniFrac.dispersion.by.HII.root.eta.squared <- F_to_eta2(
  0.007, 0.063, UniFrac.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
UniFrac.dispersion.by.HII.soil.eta.squared <- F_to_eta2(
  0.357, 0.763, UniFrac.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
UniFrac.dispersion.by.HII.effect.sizes <- tibble(
  Compartment = UniFrac.dispersion.by.HII.compartment.eta.squared,
  Smooth_by_Root = UniFrac.dispersion.by.HII.root.eta.squared,
  Smooth_by_Soil = UniFrac.dispersion.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
UniFrac.multivariate.dispersion.by.ISC.residual.df <- df.residual(
  UniFrac.multivariate.dispersion.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
UniFrac.dispersion.by.ISC.compartment.eta.squared <- F_to_eta2(
  68.4, 1, UniFrac.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
UniFrac.dispersion.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, UniFrac.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
UniFrac.dispersion.by.ISC.soil.eta.squared <- F_to_eta2(
  0.933, 2.124, UniFrac.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
UniFrac.dispersion.by.ISC.effect.sizes <- tibble(
  Compartment = UniFrac.dispersion.by.ISC.compartment.eta.squared,
  Smooth_by_Root = UniFrac.dispersion.by.ISC.root.eta.squared,
  Smooth_by_Soil = UniFrac.dispersion.by.ISC.soil.eta.squared
)
```

### UniFrac Multivariate Dispersion Effect Size Summary

Table 6: Summary of effect sizes (partial eta-squared) for the UniFrac multivariate dispersion GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.50151	0e+00	0.00000
HII	0.51629	1e-05	0.00404
ISC	0.50940	0e+00	0.02920

## Weighted UniFrac Distance

### Distance

```
## Get model residuals
weighted.UniFrac.multivariate.dispersion.by.distance.residual.df <- df.residual(
  weighted.UniFrac.multivariate.dispersion.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
weighted.UniFrac.dispersion.by.distance.compartment.eta.squared <- F_to_eta2(
  122.4, 1, weighted.UniFrac.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
weighted.UniFrac.dispersion.by.distance.root.eta.squared <- F_to_eta2(
  1.122, 2.255, weighted.UniFrac.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
weighted.UniFrac.dispersion.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, weighted.UniFrac.multivariate.dispersion.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
weighted.UniFrac.dispersion.by.distance.effect.sizes <- tibble(
  Compartment = weighted.UniFrac.dispersion.by.distance.compartment.eta.squared,
  Smooth_by_Root = weighted.UniFrac.dispersion.by.distance.root.eta.squared,
  Smooth_by_Soil = weighted.UniFrac.dispersion.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
weighted.UniFrac.multivariate.dispersion.by.HII.residual.df <- df.residual(
  weighted.UniFrac.multivariate.dispersion.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
weighted.UniFrac.dispersion.by.HII.compartment.eta.squared <- F_to_eta2(
  106.6, 1, weighted.UniFrac.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
weighted.UniFrac.dispersion.by.HII.root.eta.squared <- F_to_eta2(
  0.001, 0.00001, weighted.UniFrac.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
weighted.UniFrac.dispersion.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, weighted.UniFrac.multivariate.dispersion.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
weighted.UniFrac.dispersion.by.HII.effect.sizes <- tibble(
  Compartment = weighted.UniFrac.dispersion.by.HII.compartment.eta.squared,
  Smooth_by_Root = weighted.UniFrac.dispersion.by.HII.root.eta.squared,
  Smooth_by_Soil = weighted.UniFrac.dispersion.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
weighted.UniFrac.multivariate.dispersion.by.ISC.residual.df <- df.residual(
  weighted.UniFrac.multivariate.dispersion.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
weighted.UniFrac.dispersion.by.ISC.compartment.eta.squared <- F_to_eta2(
  106.6, 1, weighted.UniFrac.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
weighted.UniFrac.dispersion.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, weighted.UniFrac.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
weighted.UniFrac.dispersion.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, weighted.UniFrac.multivariate.dispersion.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
weighted.UniFrac.dispersion.by.ISC.effect.sizes <- tibble(
  Compartment = weighted.UniFrac.dispersion.by.ISC.compartment.eta.squared,
  Smooth_by_Root = weighted.UniFrac.dispersion.by.ISC.root.eta.squared,
  Smooth_by_Soil = weighted.UniFrac.dispersion.by.ISC.soil.eta.squared
)
```

## Weighted UniFrac Multivariate Dispersion Effect Size Summary

Table 7: Summary of effect sizes (partial eta-squared) for the weighted UniFrac multivariate dispersion GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.65056	0.03706	0
HII	0.61054	0.00000	0
ISC	0.61054	0.00000	0

# Mutualistic Bacteria

## Allorhizobium

### Distance

```
## Get model residuals
allorhizobium.by.distance.residual.df <- df.residual(
  allorhizobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
allorhizobium.by.distance.compartment.eta.squared <- F_to_eta2(
  12.7, 1, allorhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

# Smooth of distance by root
allorhizobium.by.distance.root.eta.squared <- F_to_eta2(
  2.535, 2.644, allorhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

# Smooth of distance by soil
allorhizobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, allorhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
allorhizobium.by.distance.effect.sizes <- tibble(
  Compartment = allorhizobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = allorhizobium.by.distance.root.eta.squared,
  Smooth_by_Soil = allorhizobium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
allorhizobium.by.HII.residual.df <- df.residual(
  allorhizobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
allorhizobium.by.HII.compartment.eta.squared <- F_to_eta2(
  10.8, 1, allorhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
allorhizobium.by.HII.root.eta.squared <- F_to_eta2(
  1.051, 0.905, allorhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
allorhizobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, allorhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
allorhizobium.by.HII.effect.sizes <- tibble(
  Compartment = allorhizobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = allorhizobium.by.HII.root.eta.squared,
  Smooth_by_Soil = allorhizobium.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
allorhizobium.by.ISC.residual.df <- df.residual(
  allorhizobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
allorhizobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  9.781, 1, allorhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
allorhizobium.by.ISC.root.eta.squared <- F_to_eta2(
  0.215, 0.671, allorhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
allorhizobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, allorhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
allorhizobium.by.ISC.effect.sizes <- tibble(
  Compartment = allorhizobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = allorhizobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = allorhizobium.by.ISC.soil.eta.squared
)
```

### Allorhizobium Effect Size Summary

Table 8: Summary of effect sizes (partial eta-squared) for the Allorhizobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.16271	0.09302	0
HII	0.13865	0.01398	0
ISC	0.12685	0.00214	0

## Bradyrhizobium

### Distance

```
## Get model residuals
bradyrhizobium.by.distance.residual.df <- df.residual(
  bradyrhizobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
bradyrhizobium.by.distance.compartment.eta.squared <- F_to_eta2(
  36.4, 1, bradyrhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
bradyrhizobium.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, bradyrhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
bradyrhizobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.589, 1.894, bradyrhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
bradyrhizobium.by.distance.effect.sizes <- tibble(
  Compartment = bradyrhizobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = bradyrhizobium.by.distance.root.eta.squared,
  Smooth_by_Soil = bradyrhizobium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
bradyrhizobium.by.HII.residual.df <- df.residual(
  bradyrhizobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
bradyrhizobium.by.HII.compartment.eta.squared <- F_to_eta2(
  33.8, 1, bradyrhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
bradyrhizobium.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, bradyrhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
bradyrhizobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, bradyrhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
bradyrhizobium.by.HII.effect.sizes <- tibble(
  Compartment = bradyrhizobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = bradyrhizobium.by.HII.root.eta.squared,
  Smooth_by_Soil = bradyrhizobium.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
bradyrhizobium.by.ISC.residual.df <- df.residual(
  bradyrhizobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
bradyrhizobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  36.6, 1, bradyrhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
bradyrhizobium.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, bradyrhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
bradyrhizobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.634, 1.948, bradyrhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
bradyrhizobium.by.ISC.effect.sizes <- tibble(
  Compartment = bradyrhizobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = bradyrhizobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = bradyrhizobium.by.ISC.soil.eta.squared
)
```

## Bradyrhizobium Effect Size Summary

Table 9: Summary of effect sizes (partial eta-squared) for the Bradyrhizobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.35510	0	0.01660
HII	0.33202	0	0.00000
ISC	0.35655	0	0.01835

## Mesorhizobium

### Distance

```
## Get model residuals
mesorhizobium.by.distance.residual.df <- df.residual(
  mesorhizobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
mesorhizobium.by.distance.compartment.eta.squared <- F_to_eta2(
  33.1, 1, mesorhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
mesorhizobium.by.distance.root.eta.squared <- F_to_eta2(
  0.043, 0.278, mesorhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
mesorhizobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, mesorhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
mesorhizobium.by.distance.effect.sizes <- tibble(
  Compartment = mesorhizobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = mesorhizobium.by.distance.root.eta.squared,
  Smooth_by_Soil = mesorhizobium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
mesorhizobium.by.HII.residual.df <- df.residual(
  mesorhizobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
mesorhizobium.by.HII.compartment.eta.squared <- F_to_eta2(
  37.0, 1, mesorhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
mesorhizobium.by.HII.root.eta.squared <- F_to_eta2(
  0.005, 0.046, mesorhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
mesorhizobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.936, 2.229, mesorhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
mesorhizobium.by.HII.effect.sizes <- tibble(
  Compartment = mesorhizobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = mesorhizobium.by.HII.root.eta.squared,
  Smooth_by_Soil = mesorhizobium.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
mesorhizobium.by.ISC.residual.df <- df.residual(
  mesorhizobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
mesorhizobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  33.4, 1, mesorhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
mesorhizobium.by.ISC.root.eta.squared <- F_to_eta2(
  0.11, 0.5, mesorhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
mesorhizobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, mesorhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
mesorhizobium.by.ISC.effect.sizes <- tibble(
  Compartment = mesorhizobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = mesorhizobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = mesorhizobium.by.ISC.soil.eta.squared
)
```

## Mesorhizobium Effect Size Summary

Table 10: Summary of effect sizes (partial eta-squared) for the Mesorhizobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.32830	0.00018	0.00000
HII	0.36019	0.00000	0.03077
ISC	0.33102	0.00081	0.00000

## Pararhizobium

### Distance

```
## Get model residuals
pararhizobium.by.distance.residual.df <- df.residual(
  pararhizobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
pararhizobium.by.distance.compartment.eta.squared <- F_to_eta2(
  142.8, 1, pararhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
pararhizobium.by.distance.root.eta.squared <- F_to_eta2(
  0.172, 0.612, pararhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
pararhizobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, pararhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
pararhizobium.by.distance.effect.sizes <- tibble(
  Compartment = pararhizobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = pararhizobium.by.distance.root.eta.squared,
  Smooth_by_Soil = pararhizobium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
pararhizobium.by.HII.residual.df <- df.residual(
  pararhizobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
pararhizobium.by.HII.compartment.eta.squared <- F_to_eta2(
  141.2, 1, pararhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
pararhizobium.by.HII.root.eta.squared <- F_to_eta2(
  0.082, 0.424, pararhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
pararhizobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, pararhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
pararhizobium.by.HII.effect.sizes <- tibble(
  Compartment = pararhizobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = pararhizobium.by.HII.root.eta.squared,
  Smooth_by_Soil = pararhizobium.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
pararhizobium.by.ISC.residual.df <- df.residual(
  pararhizobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
pararhizobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  140.8, 1, pararhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
pararhizobium.by.ISC.root.eta.squared <- F_to_eta2(
  0.061, 0.357, pararhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
pararhizobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, pararhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
pararhizobium.by.ISC.effect.sizes <- tibble(
  Compartment = pararhizobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = pararhizobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = pararhizobium.by.ISC.soil.eta.squared
)
```

### Pararhizobium Effect Size Summary

Table 11: Summary of effect sizes (partial eta-squared) for the Pararhizobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.67939	0.00156	0
HII	0.67632	0.00051	0
ISC	0.67548	0.00032	0

## Rhizobium

### Distance

```
## Get model residuals
rhizobium.by.distance.residual.df <- df.residual(
  rhizobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
rhizobium.by.distance.compartment.eta.squared <- F_to_eta2(
  109.3, 1, rhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
rhizobium.by.distance.root.eta.squared <- F_to_eta2(
  1.956, 3.196, rhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
rhizobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, rhizobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
rhizobium.by.distance.effect.sizes <- tibble(
  Compartment = rhizobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = rhizobium.by.distance.root.eta.squared,
  Smooth_by_Soil = rhizobium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
rhizobium.by.HII.residual.df <- df.residual(
  rhizobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
rhizobium.by.HII.compartment.eta.squared <- F_to_eta2(
  88.7, 1, rhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
rhizobium.by.HII.root.eta.squared <- F_to_eta2(
  0.165, 0.598, rhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
rhizobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, rhizobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
rhizobium.by.HII.effect.sizes <- tibble(
  Compartment = rhizobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = rhizobium.by.HII.root.eta.squared,
  Smooth_by_Soil = rhizobium.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
rhizobium.by.ISC.residual.df <- df.residual(
  rhizobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
rhizobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  145.6, 1, rhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
rhizobium.by.ISC.root.eta.squared <- F_to_eta2(
  5.115, 5.959, rhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
rhizobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, rhizobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
rhizobium.by.ISC.effect.sizes <- tibble(
  Compartment = rhizobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = rhizobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = rhizobium.by.ISC.soil.eta.squared
)
```

## Rhizobium Effect Size Summary

Table 12: Summary of effect sizes (partial eta-squared) for the Rhizobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.62778	0.08798	0
HII	0.56822	0.00146	0
ISC	0.70121	0.32944	0

## Shinella

### Distance

```
## Get model residuals
shinella.by.distance.residual.df <- df.residual(
  shinella.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
shinella.by.distance.compartment.eta.squared <- F_to_eta2(
  40.2, 1, shinella.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
shinella.by.distance.root.eta.squared <- F_to_eta2(
  0.579, 0.869, shinella.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
shinella.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, shinella.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
shinella.by.distance.effect.sizes <- tibble(
  Compartment = shinella.by.distance.compartment.eta.squared,
  Smooth_by_Root = shinella.by.distance.root.eta.squared,
  Smooth_by_Soil = shinella.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
shinella.by.HII.residual.df <- df.residual(
  shinella.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
shinella.by.HII.compartment.eta.squared <- F_to_eta2(
  42.9, 1, shinella.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
shinella.by.HII.root.eta.squared <- F_to_eta2(
  1.138, 0.911, shinella.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
shinella.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, shinella.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
shinella.by.HII.effect.sizes <- tibble(
  Compartment = shinella.by.HII.compartment.eta.squared,
  Smooth_by_Root = shinella.by.HII.root.eta.squared,
  Smooth_by_Soil = shinella.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
shinella.by.ISC.residual.df <- df.residual(
  shinella.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
shinella.by.ISC.compartment.eta.squared <- F_to_eta2(
  38.6, 1, shinella.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
shinella.by.ISC.root.eta.squared <- F_to_eta2(
  0.250, 0.708, shinella.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
shinella.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, shinella.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
shinella.by.ISC.effect.sizes <- tibble(
  Compartment = shinella.by.ISC.compartment.eta.squared,
  Smooth_by_Root = shinella.by.ISC.root.eta.squared,
  Smooth_by_Soil = shinella.by.ISC.soil.eta.squared
)
```

## Shinella Effect Size Summary

Table 13: Summary of effect sizes (partial eta-squared) for the Shinella abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.37454	0.00744	0
HII	0.39004	0.01522	0
ISC	0.36452	0.00262	0

# Pathogenic Bacteria

## Legionella

### Distance

```
## Get model residuals
legionella.by.distance.residual.df <- df.residual(
  legionella.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
legionella.by.distance.compartment.eta.squared <- F_to_eta2(
  32.59, 1, legionella.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

# Smooth of distance by root
legionella.by.distance.root.eta.squared <- F_to_eta2(
  0.166, 0.60, legionella.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

# Smooth of distance by soil
legionella.by.distance.soil.eta.squared <- F_to_eta2(
  0.082, 0.43, legionella.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
legionella.by.distance.effect.sizes <- tibble(
  Compartment = legionella.by.distance.compartment.eta.squared,
  Smooth_by_Root = legionella.by.distance.root.eta.squared,
  Smooth_by_Soil = legionella.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
legionella.by.HII.residual.df <- df.residual(
  legionella.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
legionella.by.HII.compartment.eta.squared <- F_to_eta2(
  31.77, 1, legionella.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
legionella.by.HII.root.eta.squared <- F_to_eta2(
  0.051, 0.313, legionella.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
legionella.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.0002, legionella.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
legionella.by.HII.effect.sizes <- tibble(
  Compartment = legionella.by.HII.compartment.eta.squared,
  Smooth_by_Root = legionella.by.HII.root.eta.squared,
  Smooth_by_Soil = legionella.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
legionella.by.ISC.residual.df <- df.residual(
  legionella.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
legionella.by.ISC.compartment.eta.squared <- F_to_eta2(
  32.89, 1, legionella.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
legionella.by.ISC.root.eta.squared <- F_to_eta2(
  0.138, 0.556, legionella.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
legionella.by.ISC.soil.eta.squared <- F_to_eta2(
  0.182, 0.631, legionella.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
legionella.by.ISC.effect.sizes <- tibble(
  Compartment = legionella.by.ISC.compartment.eta.squared,
  Smooth_by_Root = legionella.by.ISC.root.eta.squared,
  Smooth_by_Soil = legionella.by.ISC.soil.eta.squared
)
```

## Legionella Effect Size Summary

Table 14: Summary of effect sizes (partial eta-squared) for the Legionella abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.32735	0.00149	0.00053
HII	0.31943	0.00024	0.00000
ISC	0.32988	0.00115	0.00172

## Mycobacterium

### Distance

```
## Get model residuals
mycobacterium.by.distance.residual.df <- df.residual(
  mycobacterium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
mycobacterium.by.distance.compartment.eta.squared <- F_to_eta2(
  100, 1, mycobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
mycobacterium.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, mycobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
mycobacterium.by.distance.soil.eta.squared <- F_to_eta2(
  0.122, 0.526, mycobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
mycobacterium.by.distance.effect.sizes <- tibble(
  Compartment = mycobacterium.by.distance.compartment.eta.squared,
  Smooth_by_Root = mycobacterium.by.distance.root.eta.squared,
  Smooth_by_Soil = mycobacterium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
mycobacterium.by.HII.residual.df <- df.residual(
  mycobacterium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
mycobacterium.by.HII.compartment.eta.squared <- F_to_eta2(
  99.4, 1, mycobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
mycobacterium.by.HII.root.eta.squared <- F_to_eta2(
  0.058, 0.345, mycobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
mycobacterium.by.HII.soil.eta.squared <- F_to_eta2(
  0.013, 0.105, mycobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
mycobacterium.by.HII.effect.sizes <- tibble(
  Compartment = mycobacterium.by.HII.compartment.eta.squared,
  Smooth_by_Root = mycobacterium.by.HII.root.eta.squared,
  Smooth_by_Soil = mycobacterium.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
mycobacterium.by.ISC.residual.df <- df.residual(
  mycobacterium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
mycobacterium.by.ISC.compartment.eta.squared <- F_to_eta2(
  98.5, 1, mycobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
mycobacterium.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, mycobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
mycobacterium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.008, 0.067, mycobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
mycobacterium.by.ISC.effect.sizes <- tibble(
  Compartment = mycobacterium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = mycobacterium.by.ISC.root.eta.squared,
  Smooth_by_Soil = mycobacterium.by.ISC.soil.eta.squared
)
```

## Mycobacterium Effect Size Summary

Table 15: Summary of effect sizes (partial eta-squared) for the Mycobacterium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.59711	0e+00	0.00095
HII	0.59539	3e-04	0.00002
ISC	0.59183	0e+00	0.00001

## Staphylococcus

### Distance

```
## Get model residuals
staphylococcus.by.distance.residual.df <- df.residual(
  staphylococcus.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
staphylococcus.by.distance.compartment.eta.squared <- F_to_eta2(
  1.836, 1, staphylococcus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
staphylococcus.by.distance.root.eta.squared <- F_to_eta2(
  0.924, 1.91, staphylococcus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
staphylococcus.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, staphylococcus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
staphylococcus.by.distance.effect.sizes <- tibble(
  Compartment = staphylococcus.by.distance.compartment.eta.squared,
  Smooth_by_Root = staphylococcus.by.distance.root.eta.squared,
  Smooth_by_Soil = staphylococcus.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
staphylococcus.by.HII.residual.df <- df.residual(
  staphylococcus.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
staphylococcus.by.HII.compartment.eta.squared <- F_to_eta2(
  2.717, 1, staphylococcus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
staphylococcus.by.HII.root.eta.squared <- F_to_eta2(
  4.989, 3.523, staphylococcus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
staphylococcus.by.HII.soil.eta.squared <- F_to_eta2(
  0.936, 2.229, staphylococcus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
staphylococcus.by.HII.effect.sizes <- tibble(
  Compartment = staphylococcus.by.HII.compartment.eta.squared,
  Smooth_by_Root = staphylococcus.by.HII.root.eta.squared,
  Smooth_by_Soil = staphylococcus.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
staphylococcus.by.ISC.residual.df <- df.residual(
  staphylococcus.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
staphylococcus.by.ISC.compartment.eta.squared <- F_to_eta2(
  1.67, 1, staphylococcus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
staphylococcus.by.ISC.root.eta.squared <- F_to_eta2(
  0.154, 0.586, staphylococcus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
staphylococcus.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, staphylococcus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
staphylococcus.by.ISC.effect.sizes <- tibble(
  Compartment = staphylococcus.by.ISC.compartment.eta.squared,
  Smooth_by_Root = staphylococcus.by.ISC.root.eta.squared,
  Smooth_by_Soil = staphylococcus.by.ISC.soil.eta.squared
)
```

## Staphylococcus Effect Size Summary

Table 16: Summary of effect sizes (partial eta-squared) for the Staphylococcus abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.02703	0.02601	0.00000
HII	0.04044	0.21421	0.03134
ISC	0.02417	0.00134	0.00000

## Stenotrophomonas

### Distance

```
## Get model residuals
stenotrophomonas.by.distance.residual.df <- df.residual(
  stenotrophomonas.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
stenotrophomonas.by.distance.compartment.eta.squared <- F_to_eta2(
  21.2, 1, stenotrophomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
stenotrophomonas.by.distance.root.eta.squared <- F_to_eta2(
  0.404, 0.799, stenotrophomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
stenotrophomonas.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, stenotrophomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
stenotrophomonas.by.distance.effect.sizes <- tibble(
  Compartment = stenotrophomonas.by.distance.compartment.eta.squared,
  Smooth_by_Root = stenotrophomonas.by.distance.root.eta.squared,
  Smooth_by_Soil = stenotrophomonas.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
stenotrophomonas.by.HII.residual.df <- df.residual(
  stenotrophomonas.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
stenotrophomonas.by.HII.compartment.eta.squared <- F_to_eta2(
  20.3, 1, stenotrophomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
stenotrophomonas.by.HII.root.eta.squared <- F_to_eta2(
  0.165, 0.598, stenotrophomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
stenotrophomonas.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, stenotrophomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
stenotrophomonas.by.HII.effect.sizes <- tibble(
  Compartment = stenotrophomonas.by.HII.compartment.eta.squared,
  Smooth_by_Root = stenotrophomonas.by.HII.root.eta.squared,
  Smooth_by_Soil = stenotrophomonas.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
stenotrophomonas.by.ISC.residual.df <- df.residual(
  stenotrophomonas.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
stenotrophomonas.by.ISC.compartment.eta.squared <- F_to_eta2(
  20.8, 1, stenotrophomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
stenotrophomonas.by.ISC.root.eta.squared <- F_to_eta2(
  0.248, 0.697, stenotrophomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
stenotrophomonas.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, stenotrophomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
stenotrophomonas.by.ISC.effect.sizes <- tibble(
  Compartment = stenotrophomonas.by.ISC.compartment.eta.squared,
  Smooth_by_Root = stenotrophomonas.by.ISC.root.eta.squared,
  Smooth_by_Soil = stenotrophomonas.by.ISC.soil.eta.squared
)
```

## Stenotrophomonas Effect Size Summary

Table 17: Summary of effect sizes (partial eta-squared) for the Stenotrophomonas abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.23982	0.00478	0
HII	0.23096	0.00146	0
ISC	0.23609	0.00256	0

## Acinetobacter

### Distance

```
## Get model residuals
acinetobacter.by.distance.residual.df <- df.residual(
  acinetobacter.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
acinetobacter.by.distance.compartment.eta.squared <- F_to_eta2(
  2.542, 1, acinetobacter.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
acinetobacter.by.distance.root.eta.squared <- F_to_eta2(
  0.581, 0.864, acinetobacter.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
acinetobacter.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.001, acinetobacter.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
acinetobacter.by.distance.effect.sizes <- tibble(
  Compartment = acinetobacter.by.distance.compartment.eta.squared,
  Smooth_by_Root = acinetobacter.by.distance.root.eta.squared,
  Smooth_by_Soil = acinetobacter.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
acinetobacter.by.HII.residual.df <- df.residual(
  acinetobacter.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
acinetobacter.by.HII.compartment.eta.squared <- F_to_eta2(
  2.381, 1, acinetobacter.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
acinetobacter.by.HII.root.eta.squared <- F_to_eta2(
  0.068, 0.379, acinetobacter.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
acinetobacter.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.001, acinetobacter.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
acinetobacter.by.HII.effect.sizes <- tibble(
  Compartment = acinetobacter.by.HII.compartment.eta.squared,
  Smooth_by_Root = acinetobacter.by.HII.root.eta.squared,
  Smooth_by_Soil = acinetobacter.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
acinetobacter.by.ISC.residual.df <- df.residual(
  acinetobacter.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
acinetobacter.by.ISC.compartment.eta.squared <- F_to_eta2(
  2.476, 1, acinetobacter.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
acinetobacter.by.ISC.root.eta.squared <- F_to_eta2(
  0.369, 0.779, acinetobacter.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
acinetobacter.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, acinetobacter.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
acinetobacter.by.ISC.effect.sizes <- tibble(
  Compartment = acinetobacter.by.ISC.compartment.eta.squared,
  Smooth_by_Root = acinetobacter.by.ISC.root.eta.squared,
  Smooth_by_Soil = acinetobacter.by.ISC.soil.eta.squared
)
```

### Acinetobacter Effect Size Summary

Table 18: Summary of effect sizes (partial eta-squared) for the Acinetobacter abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.03648	0.00742	0
HII	0.03401	0.00038	0
ISC	0.03553	0.00426	0

## Clostridium

### Distance

```
## Get model residuals
clostridium.by.distance.residual.df <- df.residual(
  clostridium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
clostridium.by.distance.compartment.eta.squared <- F_to_eta2(
  68.9, 1, clostridium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
clostridium.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, clostridium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
clostridium.by.distance.soil.eta.squared <- F_to_eta2(
  0.771, 0.902, clostridium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
clostridium.by.distance.effect.sizes <- tibble(
  Compartment = clostridium.by.distance.compartment.eta.squared,
  Smooth_by_Root = clostridium.by.distance.root.eta.squared,
  Smooth_by_Soil = clostridium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
clostridium.by.HII.residual.df <- df.residual(
  clostridium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
clostridium.by.HII.compartment.eta.squared <- F_to_eta2(
  63.4, 1, clostridium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
clostridium.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, clostridium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
clostridium.by.HII.soil.eta.squared <- F_to_eta2(
  0.107, 0.492, clostridium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
clostridium.by.HII.effect.sizes <- tibble(
  Compartment = clostridium.by.HII.compartment.eta.squared,
  Smooth_by_Root = clostridium.by.HII.root.eta.squared,
  Smooth_by_Soil = clostridium.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
clostridium.by.ISC.residual.df <- df.residual(
  clostridium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
clostridium.by.ISC.compartment.eta.squared <- F_to_eta2(
  66.9, 1, clostridium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
clostridium.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, clostridium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
clostridium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.522, 0.843, clostridium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
clostridium.by.ISC.effect.sizes <- tibble(
  Compartment = clostridium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = clostridium.by.ISC.root.eta.squared,
  Smooth_by_Soil = clostridium.by.ISC.soil.eta.squared
)
```

### Clostridium Effect Size Summary

Table 19: Summary of effect sizes (partial eta-squared) for the Clostridium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.50663	0	0.01026
HII	0.48431	0	0.00078
ISC	0.49904	0	0.00651

## Paenibacillus

### Distance

```
## Get model residuals
paenibacillus.by.distance.residual.df <- df.residual(
  paenibacillus.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
paenibacillus.by.distance.compartment.eta.squared <- F_to_eta2(
  39.8, 1, paenibacillus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
paenibacillus.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.0001, paenibacillus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
paenibacillus.by.distance.soil.eta.squared <- F_to_eta2(
  0.726, 0.892, paenibacillus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
paenibacillus.by.distance.effect.sizes <- tibble(
  Compartment = paenibacillus.by.distance.compartment.eta.squared,
  Smooth_by_Root = paenibacillus.by.distance.root.eta.squared,
  Smooth_by_Soil = paenibacillus.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
paenibacillus.by.HII.residual.df <- df.residual(
  paenibacillus.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
paenibacillus.by.HII.compartment.eta.squared <- F_to_eta2(
  39.2, 1, paenibacillus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
paenibacillus.by.HII.root.eta.squared <- F_to_eta2(
  0.179, 0.617, paenibacillus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
paenibacillus.by.HII.soil.eta.squared <- F_to_eta2(
  0.428, 0.794, paenibacillus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
paenibacillus.by.HII.effect.sizes <- tibble(
  Compartment = paenibacillus.by.HII.compartment.eta.squared,
  Smooth_by_Root = paenibacillus.by.HII.root.eta.squared,
  Smooth_by_Soil = paenibacillus.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
paenibacillus.by.ISC.residual.df <- df.residual(
  paenibacillus.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
paenibacillus.by.ISC.compartment.eta.squared <- F_to_eta2(
  36.9, 1, paenibacillus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
paenibacillus.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, paenibacillus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
paenibacillus.by.ISC.soil.eta.squared <- F_to_eta2(
  0.121, 0.526, paenibacillus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
paenibacillus.by.ISC.effect.sizes <- tibble(
  Compartment = paenibacillus.by.ISC.compartment.eta.squared,
  Smooth_by_Root = paenibacillus.by.ISC.root.eta.squared,
  Smooth_by_Soil = paenibacillus.by.ISC.soil.eta.squared
)
```

## Paenibacillus Effect Size Summary

Table 20: Summary of effect sizes (partial eta-squared) for the Paenibacillus abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.37228	0.00000	0.00956
HII	0.37055	0.00166	0.00508
ISC	0.35354	0.00000	0.00094

## Williamsia

### Distance

```
## Get model residuals
williamsia.by.distance.residual.df <- df.residual(
  williamsia.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
williamsia.by.distance.compartment.eta.squared <- F_to_eta2(
  0.914, 1, williamsia.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
williamsia.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, williamsia.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
williamsia.by.distance.soil.eta.squared <- F_to_eta2(
  0.312, 0.749, williamsia.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
williamsia.by.distance.effect.sizes <- tibble(
  Compartment = williamsia.by.distance.compartment.eta.squared,
  Smooth_by_Root = williamsia.by.distance.root.eta.squared,
  Smooth_by_Soil = williamsia.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
williamsia.by.HII.residual.df <- df.residual(
  williamsia.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
williamsia.by.HII.compartment.eta.squared <- F_to_eta2(
  0.920, 1, williamsia.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
williamsia.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, williamsia.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
williamsia.by.HII.soil.eta.squared <- F_to_eta2(
  0.360, 0.764, williamsia.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
williamsia.by.HII.effect.sizes <- tibble(
  Compartment = williamsia.by.HII.compartment.eta.squared,
  Smooth_by_Root = williamsia.by.HII.root.eta.squared,
  Smooth_by_Soil = williamsia.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
williamsia.by.ISC.residual.df <- df.residual(
  williamsia.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
williamsia.by.ISC.compartment.eta.squared <- F_to_eta2(
  0.901, 1, williamsia.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
williamsia.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, williamsia.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
williamsia.by.ISC.soil.eta.squared <- F_to_eta2(
  0.193, 0.639, williamsia.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
williamsia.by.ISC.effect.sizes <- tibble(
  Compartment = williamsia.by.ISC.compartment.eta.squared,
  Smooth_by_Root = williamsia.by.ISC.root.eta.squared,
  Smooth_by_Soil = williamsia.by.ISC.soil.eta.squared
)
```

## Williamsia Effect Size Summary

Table 21: Summary of effect sizes (partial eta-squared) for the Williamsia abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.01341	0	0.00346
HII	0.01350	0	0.00407
ISC	0.01320	0	0.00183

## Sphingomonas

### Distance

```
## Get model residuals
sphingomonas.by.distance.residual.df <- df.residual(
  sphingomonas.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingomonas.by.distance.compartment.eta.squared <- F_to_eta2(
  76.4, 1, sphingomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
sphingomonas.by.distance.root.eta.squared <- F_to_eta2(
  2.365, 2.433, sphingomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
sphingomonas.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingomonas.by.distance.effect.sizes <- tibble(
  Compartment = sphingomonas.by.distance.compartment.eta.squared,
  Smooth_by_Root = sphingomonas.by.distance.root.eta.squared,
  Smooth_by_Soil = sphingomonas.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
sphingomonas.by.HII.residual.df <- df.residual(
  sphingomonas.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingomonas.by.HII.compartment.eta.squared <- F_to_eta2(
  58.2, 1, sphingomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
sphingomonas.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
sphingomonas.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingomonas.by.HII.effect.sizes <- tibble(
  Compartment = sphingomonas.by.HII.compartment.eta.squared,
  Smooth_by_Root = sphingomonas.by.HII.root.eta.squared,
  Smooth_by_Soil = sphingomonas.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
sphingomonas.by.ISC.residual.df <- df.residual(
  sphingomonas.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingomonas.by.ISC.compartment.eta.squared <- F_to_eta2(
  58.2, 1, sphingomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
sphingomonas.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
sphingomonas.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingomonas.by.ISC.effect.sizes <- tibble(
  Compartment = sphingomonas.by.ISC.compartment.eta.squared,
  Smooth_by_Root = sphingomonas.by.ISC.root.eta.squared,
  Smooth_by_Soil = sphingomonas.by.ISC.soil.eta.squared
)
```

## Sphingomonas Effect Size Summary

Table 22: Summary of effect sizes (partial eta-squared) for the Sphingomonas abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.53816	0.08068	0
HII	0.46117	0.00000	0
ISC	0.46117	0.00000	0

## Xanthomonas

### Distance

```
## Get model residuals
xanthomonas.by.distance.residual.df <- df.residual(
  xanthomonas.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
xanthomonas.by.distance.compartment.eta.squared <- F_to_eta2(
  18.2, 1, xanthomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
xanthomonas.by.distance.root.eta.squared <- F_to_eta2(
  0.656, 0.886, xanthomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
xanthomonas.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, xanthomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
xanthomonas.by.distance.effect.sizes <- tibble(
  Compartment = xanthomonas.by.distance.compartment.eta.squared,
  Smooth_by_Root = xanthomonas.by.distance.root.eta.squared,
  Smooth_by_Soil = xanthomonas.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
xanthomonas.by.HII.residual.df <- df.residual(
  xanthomonas.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
xanthomonas.by.HII.compartment.eta.squared <- F_to_eta2(
  19.6, 1, xanthomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
xanthomonas.by.HII.root.eta.squared <- F_to_eta2(
  1.302, 0.922, xanthomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
xanthomonas.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, xanthomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
xanthomonas.by.HII.effect.sizes <- tibble(
  Compartment = xanthomonas.by.HII.compartment.eta.squared,
  Smooth_by_Root = xanthomonas.by.HII.root.eta.squared,
  Smooth_by_Soil = xanthomonas.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
xanthomonas.by.ISC.residual.df <- df.residual(
  xanthomonas.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
xanthomonas.by.ISC.compartment.eta.squared <- F_to_eta2(
  17.8, 1, xanthomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
xanthomonas.by.ISC.root.eta.squared <- F_to_eta2(
  0.480, 0.834, xanthomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
xanthomonas.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, xanthomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
xanthomonas.by.ISC.effect.sizes <- tibble(
  Compartment = xanthomonas.by.ISC.compartment.eta.squared,
  Smooth_by_Root = xanthomonas.by.ISC.root.eta.squared,
  Smooth_by_Soil = xanthomonas.by.ISC.soil.eta.squared
)
```

## Xanthomonas Effect Size Summary

Table 23: Summary of effect sizes (partial eta-squared) for the Xanthomonas abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.21333	0.00859	0
HII	0.22612	0.01758	0
ISC	0.20950	0.00592	0

## Rhizobacter

### Distance

```
## Get model residuals
rhizobacter.by.distance.residual.df <- df.residual(
  rhizobacter.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
rhizobacter.by.distance.compartment.eta.squared <- F_to_eta2(
  115.9, 1, rhizobacter.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
rhizobacter.by.distance.root.eta.squared <- F_to_eta2(
  1.684, 3.462, rhizobacter.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
rhizobacter.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, rhizobacter.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
rhizobacter.by.distance.effect.sizes <- tibble(
  Compartment = rhizobacter.by.distance.compartment.eta.squared,
  Smooth_by_Root = rhizobacter.by.distance.root.eta.squared,
  Smooth_by_Soil = rhizobacter.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
rhizobacter.by.HII.residual.df <- df.residual(
  rhizobacter.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
rhizobacter.by.HII.compartment.eta.squared <- F_to_eta2(
  97.8, 1, rhizobacter.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
rhizobacter.by.HII.root.eta.squared <- F_to_eta2(
  0.245, 0.688, rhizobacter.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
rhizobacter.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, rhizobacter.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
rhizobacter.by.HII.effect.sizes <- tibble(
  Compartment = rhizobacter.by.HII.compartment.eta.squared,
  Smooth_by_Root = rhizobacter.by.HII.root.eta.squared,
  Smooth_by_Soil = rhizobacter.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
rhizobacter.by.ISC.residual.df <- df.residual(
  rhizobacter.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
rhizobacter.by.ISC.compartment.eta.squared <- F_to_eta2(
  97.4, 1, rhizobacter.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
rhizobacter.by.ISC.root.eta.squared <- F_to_eta2(
  0.210, 0.660, rhizobacter.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
rhizobacter.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, rhizobacter.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
rhizobacter.by.ISC.effect.sizes <- tibble(
  Compartment = rhizobacter.by.ISC.compartment.eta.squared,
  Smooth_by_Root = rhizobacter.by.ISC.root.eta.squared,
  Smooth_by_Soil = rhizobacter.by.ISC.soil.eta.squared
)
```

## Rhizobacter Effect Size Summary

Table 24: Summary of effect sizes (partial eta-squared) for the Rhizobacter abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.64233	0.08285	0
HII	0.59233	0.00250	0
ISC	0.59123	0.00205	0

## Agrobacterium

### Distance

```
## Get model residuals
agrobacterium.by.distance.residual.df <- df.residual(
  agrobacterium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
agrobacterium.by.distance.compartment.eta.squared <- F_to_eta2(
  59.8, 1, agrobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
agrobacterium.by.distance.root.eta.squared <- F_to_eta2(
  2.438, 2.650, agrobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
agrobacterium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, agrobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
agrobacterium.by.distance.effect.sizes <- tibble(
  Compartment = agrobacterium.by.distance.compartment.eta.squared,
  Smooth_by_Root = agrobacterium.by.distance.root.eta.squared,
  Smooth_by_Soil = agrobacterium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
agrobacterium.by.HII.residual.df <- df.residual(
  agrobacterium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
agrobacterium.by.HII.compartment.eta.squared <- F_to_eta2(
  89.6, 1, agrobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
agrobacterium.by.HII.root.eta.squared <- F_to_eta2(
  7.399, 4.810, agrobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
agrobacterium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, agrobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
agrobacterium.by.HII.effect.sizes <- tibble(
  Compartment = agrobacterium.by.HII.compartment.eta.squared,
  Smooth_by_Root = agrobacterium.by.HII.root.eta.squared,
  Smooth_by_Soil = agrobacterium.by.HII.soil.eta.squared
)
```



## Mean ISC

```
## Get model residuals
agrobacterium.by.ISC.residual.df <- df.residual(
  agrobacterium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
agrobacterium.by.ISC.compartment.eta.squared <- F_to_eta2(
  52.4, 1, agrobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
agrobacterium.by.ISC.root.eta.squared <- F_to_eta2(
  1.189, 2.325, agrobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
agrobacterium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, agrobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
agrobacterium.by.ISC.effect.sizes <- tibble(
  Compartment = agrobacterium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = agrobacterium.by.ISC.root.eta.squared,
  Smooth_by_Soil = agrobacterium.by.ISC.soil.eta.squared
)
```

## Agrobacterium Effect Size Summary

Table 25: Summary of effect sizes (partial eta-squared) for the Agrobacterium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.47783	0.08997	0
HII	0.58643	0.36029	0
ISC	0.44379	0.04039	0

## Ecosystem Function Bacteria

## Nitrosomonas

### Distance

```
## Get model residuals
nitrosomonas.by.distance.residual.df <- df.residual(
  nitrosomonas.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrosomonas.by.distance.compartment.eta.squared <- F_to_eta2(
  109.3, 1, nitrosomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
nitrosomonas.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrosomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
nitrosomonas.by.distance.soil.eta.squared <- F_to_eta2(
  7.068, 2.644, nitrosomonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrosomonas.by.distance.effect.sizes <- tibble(
  Compartment = nitrosomonas.by.distance.compartment.eta.squared,
  Smooth_by_Root = nitrosomonas.by.distance.root.eta.squared,
  Smooth_by_Soil = nitrosomonas.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
nitrosomonas.by.HII.residual.df <- df.residual(
  nitrosomonas.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrosomonas.by.HII.compartment.eta.squared <- F_to_eta2(
  15.3, 1, nitrosomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
nitrosomonas.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrosomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
nitrosomonas.by.HII.soil.eta.squared <- F_to_eta2(
  0.952, 0.896, nitrosomonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrosomonas.by.HII.effect.sizes <- tibble(
  Compartment = nitrosomonas.by.HII.compartment.eta.squared,
  Smooth_by_Root = nitrosomonas.by.HII.root.eta.squared,
  Smooth_by_Soil = nitrosomonas.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
nitrosomonas.by.ISC.residual.df <- df.residual(
  nitrosomonas.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrosomonas.by.ISC.compartment.eta.squared <- F_to_eta2(
  8.9, 1, nitrosomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
nitrosomonas.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrosomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
nitrosomonas.by.ISC.soil.eta.squared <- F_to_eta2(
  1.236, 0.960, nitrosomonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrosomonas.by.ISC.effect.sizes <- tibble(
  Compartment = nitrosomonas.by.ISC.compartment.eta.squared,
  Smooth_by_Root = nitrosomonas.by.ISC.root.eta.squared,
  Smooth_by_Soil = nitrosomonas.by.ISC.soil.eta.squared
)
```

## Nitrosomonas Effect Size Summary

Table 26: Summary of effect sizes (partial eta-squared) for the Nitrosomonas abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.62580	0	0.22236
HII	0.18567	0	0.01255
ISC	0.11720	0	0.01739

## Nitrospira

### Distance

```
## Get model residuals
nitrospira.by.distance.residual.df <- df.residual(
  nitrospira.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrospira.by.distance.compartment.eta.squared <- F_to_eta2(
  354.2, 1, nitrospira.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
nitrospira.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrospira.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
nitrospira.by.distance.soil.eta.squared <- F_to_eta2(
  9.207, 2.403, nitrospira.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrospira.by.distance.effect.sizes <- tibble(
  Compartment = nitrospira.by.distance.compartment.eta.squared,
  Smooth_by_Root = nitrospira.by.distance.root.eta.squared,
  Smooth_by_Soil = nitrospira.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
nitrospira.by.HII.residual.df <- df.residual(
  nitrospira.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrospira.by.HII.compartment.eta.squared <- F_to_eta2(
  250.7, 1, nitrospira.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
nitrospira.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrospira.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
nitrospira.by.HII.soil.eta.squared <- F_to_eta2(
  4.6160, 3.051, nitrospira.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrospira.by.HII.effect.sizes <- tibble(
  Compartment = nitrospira.by.HII.compartment.eta.squared,
  Smooth_by_Root = nitrospira.by.HII.root.eta.squared,
  Smooth_by_Soil = nitrospira.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
nitrospira.by.ISC.residual.df <- df.residual(
  nitrospira.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrospira.by.ISC.compartment.eta.squared <- F_to_eta2(
  201.7, 1, nitrospira.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
nitrospira.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrospira.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
nitrospira.by.ISC.soil.eta.squared <- F_to_eta2(
  2.240, 1.018, nitrospira.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrospira.by.ISC.effect.sizes <- tibble(
  Compartment = nitrospira.by.ISC.compartment.eta.squared,
  Smooth_by_Root = nitrospira.by.ISC.root.eta.squared,
  Smooth_by_Soil = nitrospira.by.ISC.soil.eta.squared
)
```

## Nitrospira Effect Size Summary

Table 27: Summary of effect sizes (partial eta-squared) for the Nitrospira abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.84374	0	0.25221
HII	0.79424	0	0.17820
ISC	0.75070	0	0.03292

## Desulfuromonas

### Distance

```
## Get model residuals
desulfuromonas.by.distance.residual.df <- df.residual(
  desulfuromonas.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfuromonas.by.distance.compartment.eta.squared <- F_to_eta2(
  38.8, 1, desulfuromonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
desulfuromonas.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfuromonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
desulfuromonas.by.distance.soil.eta.squared <- F_to_eta2(
  2.346, 1.041, desulfuromonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfuromonas.by.distance.effect.sizes <- tibble(
  Compartment = desulfuromonas.by.distance.compartment.eta.squared,
  Smooth_by_Root = desulfuromonas.by.distance.root.eta.squared,
  Smooth_by_Soil = desulfuromonas.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
desulfuromonas.by.HII.residual.df <- df.residual(
  desulfuromonas.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfuromonas.by.HII.compartment.eta.squared <- F_to_eta2(
  34.6, 1, desulfuromonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
desulfuromonas.by.HII.root.eta.squared <- F_to_eta2(
  0.0001, 0.00001, desulfuromonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
desulfuromonas.by.HII.soil.eta.squared <- F_to_eta2(
  1.277, 0.920, desulfuromonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfuromonas.by.HII.effect.sizes <- tibble(
  Compartment = desulfuromonas.by.HII.compartment.eta.squared,
  Smooth_by_Root = desulfuromonas.by.HII.root.eta.squared,
  Smooth_by_Soil = desulfuromonas.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
desulfuromonas.by.ISC.residual.df <- df.residual(
  desulfuromonas.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfuromonas.by.ISC.compartment.eta.squared <- F_to_eta2(
  36.3, 1, desulfuromonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
desulfuromonas.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfuromonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
desulfuromonas.by.ISC.soil.eta.squared <- F_to_eta2(
  1.715, 1.003, desulfuromonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfuromonas.by.ISC.effect.sizes <- tibble(
  Compartment = desulfuromonas.by.ISC.compartment.eta.squared,
  Smooth_by_Root = desulfuromonas.by.ISC.root.eta.squared,
  Smooth_by_Soil = desulfuromonas.by.ISC.soil.eta.squared
)
```

## Desulfuromonas Effect Size Summary

Table 28: Summary of effect sizes (partial eta-squared) for the Desulfuromonas abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.36687	0	0.03519
HII	0.34028	0	0.01721
ISC	0.35142	0	0.02503

## Aciditerrimonas

### Distance

```
## Get model residuals
aciditerrimonas.by.distance.residual.df <- df.residual(
  aciditerrimonas.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
aciditerrimonas.by.distance.compartment.eta.squared <- F_to_eta2(
  42.2, 1, aciditerrimonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
aciditerrimonas.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, aciditerrimonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
aciditerrimonas.by.distance.soil.eta.squared <- F_to_eta2(
  4.109, 1.148, aciditerrimonas.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
aciditerrimonas.by.distance.effect.sizes <- tibble(
  Compartment = aciditerrimonas.by.distance.compartment.eta.squared,
  Smooth_by_Root = aciditerrimonas.by.distance.root.eta.squared,
  Smooth_by_Soil = aciditerrimonas.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
aciditerrimonas.by.HII.residual.df <- df.residual(
  aciditerrimonas.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
aciditerrimonas.by.HII.compartment.eta.squared <- F_to_eta2(
  32.6, 1, aciditerrimonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
aciditerrimonas.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, aciditerrimonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
aciditerrimonas.by.HII.soil.eta.squared <- F_to_eta2(
  1.450, 0.929, aciditerrimonas.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
aciditerrimonas.by.HII.effect.sizes <- tibble(
  Compartment = aciditerrimonas.by.HII.compartment.eta.squared,
  Smooth_by_Root = aciditerrimonas.by.HII.root.eta.squared,
  Smooth_by_Soil = aciditerrimonas.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
aciditerrimonas.by.ISC.residual.df <- df.residual(
  aciditerrimonas.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
aciditerrimonas.by.ISC.compartment.eta.squared <- F_to_eta2(
  30.8, 1, aciditerrimonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
aciditerrimonas.by.ISC.root.eta.squared <- F_to_eta2(
  0.0001, 0.00001, aciditerrimonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
aciditerrimonas.by.ISC.soil.eta.squared <- F_to_eta2(
  0.950, 0.931, aciditerrimonas.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
aciditerrimonas.by.ISC.effect.sizes <- tibble(
  Compartment = aciditerrimonas.by.ISC.compartment.eta.squared,
  Smooth_by_Root = aciditerrimonas.by.ISC.root.eta.squared,
  Smooth_by_Soil = aciditerrimonas.by.ISC.soil.eta.squared
)
```

### Aciditerrimonas Effect Size Summary

Table 29: Summary of effect sizes (partial eta-squared) for the Aciditerrimonas abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.38697	0	0.06591
HII	0.32708	0	0.01969
ISC	0.31471	0	0.01302

## Nitrosospira

### Distance

```
## Get model residuals
nitrosospira.by.distance.residual.df <- df.residual(
  nitrosospira.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrosospira.by.distance.compartment.eta.squared <- F_to_eta2(
  237.1, 1, nitrosospira.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
nitrosospira.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrosospira.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
nitrosospira.by.distance.soil.eta.squared <- F_to_eta2(
  3.362, 3.494, nitrosospira.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrosospira.by.distance.effect.sizes <- tibble(
  Compartment = nitrosospira.by.distance.compartment.eta.squared,
  Smooth_by_Root = nitrosospira.by.distance.root.eta.squared,
  Smooth_by_Soil = nitrosospira.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
nitrospira.by.HII.residual.df <- df.residual(
  nitrospira.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrospira.by.HII.compartment.eta.squared <- F_to_eta2(
  171.3, 1, nitrospira.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
nitrospira.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrospira.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
nitrospira.by.HII.soil.eta.squared <- F_to_eta2(
  0.334, 0.751, nitrospira.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrospira.by.HII.effect.sizes <- tibble(
  Compartment = nitrospira.by.HII.compartment.eta.squared,
  Smooth_by_Root = nitrospira.by.HII.root.eta.squared,
  Smooth_by_Soil = nitrospira.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
nitrospira.by.ISC.residual.df <- df.residual(
  nitrospira.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
nitrospira.by.ISC.compartment.eta.squared <- F_to_eta2(
  201.7, 1, nitrospira.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
nitrospira.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, nitrospira.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
nitrospira.by.ISC.soil.eta.squared <- F_to_eta2(
  1.730, 1.002, nitrospira.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
nitrospira.by.ISC.effect.sizes <- tibble(
  Compartment = nitrospira.by.ISC.compartment.eta.squared,
  Smooth_by_Root = nitrospira.by.ISC.root.eta.squared,
  Smooth_by_Soil = nitrospira.by.ISC.soil.eta.squared
)
```

## Nitrosospira Effect Size Summary

Table 30: Summary of effect sizes (partial eta-squared) for the Nitrosospira abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.78612	0	0.15405
HII	0.71809	0	0.00372
ISC	0.75066	0	0.02522

## Sphingopyxis

### Distance

```
## Get model residuals
sphingopyxis.by.distance.residual.df <- df.residual(
  sphingopyxis.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingopyxis.by.distance.compartment.eta.squared <- F_to_eta2(
  84.7, 1, sphingopyxis.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
sphingopyxis.by.distance.root.eta.squared <- F_to_eta2(
  0.087, 0.444, sphingopyxis.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
sphingopyxis.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingopyxis.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingopyxis.by.distance.effect.sizes <- tibble(
  Compartment = sphingopyxis.by.distance.compartment.eta.squared,
  Smooth_by_Root = sphingopyxis.by.distance.root.eta.squared,
  Smooth_by_Soil = sphingopyxis.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
sphingopyxis.by.HII.residual.df <- df.residual(
  sphingopyxis.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingopyxis.by.HII.compartment.eta.squared <- F_to_eta2(
  83.8, 1, sphingopyxis.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
sphingopyxis.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingopyxis.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
sphingopyxis.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingopyxis.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingopyxis.by.HII.effect.sizes <- tibble(
  Compartment = sphingopyxis.by.HII.compartment.eta.squared,
  Smooth_by_Root = sphingopyxis.by.HII.root.eta.squared,
  Smooth_by_Soil = sphingopyxis.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
sphingopyxis.by.ISC.residual.df <- df.residual(
  sphingopyxis.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingopyxis.by.ISC.compartment.eta.squared <- F_to_eta2(
  87.2, 1, sphingopyxis.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
sphingopyxis.by.ISC.root.eta.squared <- F_to_eta2(
  0.311, 0.750, sphingopyxis.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
sphingopyxis.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingopyxis.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingopyxis.by.ISC.effect.sizes <- tibble(
  Compartment = sphingopyxis.by.ISC.compartment.eta.squared,
  Smooth_by_Root = sphingopyxis.by.ISC.root.eta.squared,
  Smooth_by_Soil = sphingopyxis.by.ISC.soil.eta.squared
)
```

## Sphingopyxis Effect Size Summary

Table 31: Summary of effect sizes (partial eta-squared) for the Sphingopyxis abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.55630	0.00057	0
HII	0.55204	0.00000	0
ISC	0.56458	0.00346	0

## Cytophaga

### Distance

```
## Get model residuals
cytophaga.by.distance.residual.df <- df.residual(
  cytophaga.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
cytophaga.by.distance.compartment.eta.squared <- F_to_eta2(
  34.1, 1, cytophaga.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
cytophaga.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, cytophaga.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
cytophaga.by.distance.soil.eta.squared <- F_to_eta2(
  5.849, 6.008, cytophaga.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
cytophaga.by.distance.effect.sizes <- tibble(
  Compartment = cytophaga.by.distance.compartment.eta.squared,
  Smooth_by_Root = cytophaga.by.distance.root.eta.squared,
  Smooth_by_Soil = cytophaga.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
cytophaga.by.HII.residual.df <- df.residual(
  cytophaga.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
cytophaga.by.HII.compartment.eta.squared <- F_to_eta2(
  25.5, 1, cytophaga.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
cytophaga.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, cytophaga.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
cytophaga.by.HII.soil.eta.squared <- F_to_eta2(
  2.483, 0.958, cytophaga.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
cytophaga.by.HII.effect.sizes <- tibble(
  Compartment = cytophaga.by.HII.compartment.eta.squared,
  Smooth_by_Root = cytophaga.by.HII.root.eta.squared,
  Smooth_by_Soil = cytophaga.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
cytophaga.by.ISC.residual.df <- df.residual(
  cytophaga.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
cytophaga.by.ISC.compartment.eta.squared <- F_to_eta2(
  29.8, 1, cytophaga.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
cytophaga.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, cytophaga.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
cytophaga.by.ISC.soil.eta.squared <- F_to_eta2(
  4.148, 2.495, cytophaga.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
cytophaga.by.ISC.effect.sizes <- tibble(
  Compartment = cytophaga.by.ISC.compartment.eta.squared,
  Smooth_by_Root = cytophaga.by.ISC.root.eta.squared,
  Smooth_by_Soil = cytophaga.by.ISC.soil.eta.squared
)
```

## Cytophaga Effect Size Summary

Table 32: Summary of effect sizes (partial eta-squared) for the Cytophaga abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.35487	0	0.36178
HII	0.27555	0	0.03427
ISC	0.31268	0	0.13644

## Paracoccus

### Distance

```
## Get model residuals
paracoccus.by.distance.residual.df <- df.residual(
  paracoccus.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
paracoccus.by.distance.compartment.eta.squared <- F_to_eta2(
  6.6, 1, paracoccus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
paracoccus.by.distance.root.eta.squared <- F_to_eta2(
  1.064, 0.958, paracoccus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
paracoccus.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.001, paracoccus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
paracoccus.by.distance.effect.sizes <- tibble(
  Compartment = paracoccus.by.distance.compartment.eta.squared,
  Smooth_by_Root = paracoccus.by.distance.root.eta.squared,
  Smooth_by_Soil = paracoccus.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
paracoccus.by.HII.residual.df <- df.residual(
  paracoccus.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
paracoccus.by.HII.compartment.eta.squared <- F_to_eta2(
  6.2, 1, paracoccus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
paracoccus.by.HII.root.eta.squared <- F_to_eta2(
  0.552, 0.832, paracoccus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
paracoccus.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.001, paracoccus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
paracoccus.by.HII.effect.sizes <- tibble(
  Compartment = paracoccus.by.HII.compartment.eta.squared,
  Smooth_by_Root = paracoccus.by.HII.root.eta.squared,
  Smooth_by_Soil = paracoccus.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
paracoccus.by.ISC.residual.df <- df.residual(
  paracoccus.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
paracoccus.by.ISC.compartment.eta.squared <- F_to_eta2(
  7.2, 1, paracoccus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
paracoccus.by.ISC.root.eta.squared <- F_to_eta2(
  1.783, 1.021, paracoccus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
paracoccus.by.ISC.soil.eta.squared <- F_to_eta2(
  0.020, 0.152, paracoccus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
paracoccus.by.ISC.effect.sizes <- tibble(
  Compartment = paracoccus.by.ISC.compartment.eta.squared,
  Smooth_by_Root = paracoccus.by.ISC.root.eta.squared,
  Smooth_by_Soil = paracoccus.by.ISC.soil.eta.squared
)
```

## Paracoccus Effect Size Summary

Table 33: Summary of effect sizes (partial eta-squared) for the Paracoccus abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.08962	0.01498	0e+00
HII	0.08451	0.00679	0e+00
ISC	0.09726	0.02652	5e-05

## Novosphingobium

### Distance

```
## Get model residuals
novosphingobium.by.distance.residual.df <- df.residual(
  novosphingobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
novosphingobium.by.distance.compartment.eta.squared <- F_to_eta2(
  296.5, 1, novosphingobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
novosphingobium.by.distance.root.eta.squared <- F_to_eta2(
  0.279, 0.737, novosphingobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
novosphingobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, novosphingobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
novosphingobium.by.distance.effect.sizes <- tibble(
  Compartment = novosphingobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = novosphingobium.by.distance.root.eta.squared,
  Smooth_by_Soil = novosphingobium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
novosphingobium.by.HII.residual.df <- df.residual(
  novosphingobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
novosphingobium.by.HII.compartment.eta.squared <- F_to_eta2(
  285.9, 1, novosphingobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
novosphingobium.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, novosphingobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
novosphingobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, novosphingobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
novosphingobium.by.HII.effect.sizes <- tibble(
  Compartment = novosphingobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = novosphingobium.by.HII.root.eta.squared,
  Smooth_by_Soil = novosphingobium.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
novosphingobium.by.ISC.residual.df <- df.residual(
  novosphingobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
novosphingobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  287.3, 1, novosphingobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
novosphingobium.by.ISC.root.eta.squared <- F_to_eta2(
  0.036, 0.246, novosphingobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
novosphingobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, novosphingobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
novosphingobium.by.ISC.effect.sizes <- tibble(
  Compartment = novosphingobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = novosphingobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = novosphingobium.by.ISC.soil.eta.squared
)
```

## Novosphingobium Effect Size Summary

Table 34: Summary of effect sizes (partial eta-squared) for the Novosphingobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.81509	0.00305	0
HII	0.80786	0.00000	0
ISC	0.80917	0.00013	0

## Devosia

### Distance

```
## Get model residuals
devosia.by.distance.residual.df <- df.residual(
  devosia.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
devosia.by.distance.compartment.eta.squared <- F_to_eta2(
  388.3, 1, devosia.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
devosia.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, devosia.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
devosia.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, devosia.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
devosia.by.distance.effect.sizes <- tibble(
  Compartment = devosia.by.distance.compartment.eta.squared,
  Smooth_by_Root = devosia.by.distance.root.eta.squared,
  Smooth_by_Soil = devosia.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
devosia.by.HII.residual.df <- df.residual(
  devosia.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
devosia.by.HII.compartment.eta.squared <- F_to_eta2(
  391.5, 1, devosia.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
devosia.by.HII.root.eta.squared <- F_to_eta2(
  0.063, 0.361, devosia.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
devosia.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, devosia.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
devosia.by.HII.effect.sizes <- tibble(
  Compartment = devosia.by.HII.compartment.eta.squared,
  Smooth_by_Root = devosia.by.HII.root.eta.squared,
  Smooth_by_Soil = devosia.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
devosia.by.ISC.residual.df <- df.residual(
  devosia.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
devosia.by.ISC.compartment.eta.squared <- F_to_eta2(
  388.3, 1, devosia.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
devosia.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, devosia.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
devosia.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, devosia.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
devosia.by.ISC.effect.sizes <- tibble(
  Compartment = devosia.by.ISC.compartment.eta.squared,
  Smooth_by_Root = devosia.by.ISC.root.eta.squared,
  Smooth_by_Soil = devosia.by.ISC.soil.eta.squared
)
```

## Devosia Effect Size Summary

Table 35: Summary of effect sizes (partial eta-squared) for the Devosia abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.85098	0.00000	0
HII	0.85268	0.00034	0
ISC	0.85098	0.00000	0

## Streptomyces

### Distance

```
## Get model residuals
streptomyces.by.distance.residual.df <- df.residual(
  streptomyces.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
streptomyces.by.distance.compartment.eta.squared <- F_to_eta2(
  78.2, 1, streptomyces.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
streptomyces.by.distance.root.eta.squared <- F_to_eta2(
  0.192, 0.646, streptomyces.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
streptomyces.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, streptomyces.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
streptomyces.by.distance.effect.sizes <- tibble(
  Compartment = streptomyces.by.distance.compartment.eta.squared,
  Smooth_by_Root = streptomyces.by.distance.root.eta.squared,
  Smooth_by_Soil = streptomyces.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
streptomyces.by.HII.residual.df <- df.residual(
  streptomyces.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
streptomyces.by.HII.compartment.eta.squared <- F_to_eta2(
  76.2, 1, streptomyces.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
streptomyces.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, streptomyces.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
streptomyces.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, streptomyces.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
streptomyces.by.HII.effect.sizes <- tibble(
  Compartment = streptomyces.by.HII.compartment.eta.squared,
  Smooth_by_Root = streptomyces.by.HII.root.eta.squared,
  Smooth_by_Soil = streptomyces.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
streptomyces.by.ISC.residual.df <- df.residual(
  streptomyces.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
streptomyces.by.ISC.compartment.eta.squared <- F_to_eta2(
  76.2, 1, streptomyces.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
streptomyces.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, streptomyces.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
streptomyces.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, streptomyces.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
streptomyces.by.ISC.effect.sizes <- tibble(
  Compartment = streptomyces.by.ISC.compartment.eta.squared,
  Smooth_by_Root = streptomyces.by.ISC.root.eta.squared,
  Smooth_by_Soil = streptomyces.by.ISC.soil.eta.squared
)
```

## Streptomyces Effect Size Summary

Table 36: Summary of effect sizes (partial eta-squared) for the Streptomyces abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.53726	0.00184	0
HII	0.52843	0.00000	0
ISC	0.52843	0.00000	0

## Sphingobium

### Distance

```
## Get model residuals
sphingobium.by.distance.residual.df <- df.residual(
  sphingobium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingobium.by.distance.compartment.eta.squared <- F_to_eta2(
  74.6, 1, sphingobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
sphingobium.by.distance.root.eta.squared <- F_to_eta2(
  0.122, 0.528, sphingobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
sphingobium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingobium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingobium.by.distance.effect.sizes <- tibble(
  Compartment = sphingobium.by.distance.compartment.eta.squared,
  Smooth_by_Root = sphingobium.by.distance.root.eta.squared,
  Smooth_by_Soil = sphingobium.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
sphingobium.by.HII.residual.df <- df.residual(
  sphingobium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingobium.by.HII.compartment.eta.squared <- F_to_eta2(
  75.1, 1, sphingobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
sphingobium.by.HII.root.eta.squared <- F_to_eta2(
  0.176, 0.613, sphingobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
sphingobium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingobium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingobium.by.HII.effect.sizes <- tibble(
  Compartment = sphingobium.by.HII.compartment.eta.squared,
  Smooth_by_Root = sphingobium.by.HII.root.eta.squared,
  Smooth_by_Soil = sphingobium.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
sphingobium.by.ISC.residual.df <- df.residual(
  sphingobium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
sphingobium.by.ISC.compartment.eta.squared <- F_to_eta2(
  73.4, 1, sphingobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
sphingobium.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
sphingobium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, sphingobium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
sphingobium.by.ISC.effect.sizes <- tibble(
  Compartment = sphingobium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = sphingobium.by.ISC.root.eta.squared,
  Smooth_by_Soil = sphingobium.by.ISC.soil.eta.squared
)
```

## Sphingobium Effect Size Summary

Table 37: Summary of effect sizes (partial eta-squared) for the Sphingobium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.52509	0.00095	0
HII	0.52706	0.00160	0
ISC	0.51910	0.00000	0

## Desulfosporosinus

### Distance

```
## Get model residuals
desulfosporosinus.by.distance.residual.df <- df.residual(
  desulfosporosinus.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfosporosinus.by.distance.compartment.eta.squared <- F_to_eta2(
  50.0, 1, desulfosporosinus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
desulfosporosinus.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.001, desulfosporosinus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
desulfosporosinus.by.distance.soil.eta.squared <- F_to_eta2(
  0.632, 1.641, desulfosporosinus.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfosporosinus.by.distance.effect.sizes <- tibble(
  Compartment = desulfosporosinus.by.distance.compartment.eta.squared,
  Smooth_by_Root = desulfosporosinus.by.distance.root.eta.squared,
  Smooth_by_Soil = desulfosporosinus.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
desulfosporosinus.by.HII.residual.df <- df.residual(
  desulfosporosinus.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfosporosinus.by.HII.compartment.eta.squared <- F_to_eta2(
  53.4, 1, desulfosporosinus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
desulfosporosinus.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfosporosinus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
desulfosporosinus.by.HII.soil.eta.squared <- F_to_eta2(
  1.176, 2.957, desulfosporosinus.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfosporosinus.by.HII.effect.sizes <- tibble(
  Compartment = desulfosporosinus.by.HII.compartment.eta.squared,
  Smooth_by_Root = desulfosporosinus.by.HII.root.eta.squared,
  Smooth_by_Soil = desulfosporosinus.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
desulfosporosinus.by.ISC.residual.df <- df.residual(
  desulfosporosinus.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfosporosinus.by.ISC.compartment.eta.squared <- F_to_eta2(
  65.2, 1, desulfosporosinus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
desulfosporosinus.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfosporosinus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
desulfosporosinus.by.ISC.soil.eta.squared <- F_to_eta2(
  3.111, 5.460, desulfosporosinus.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfosporosinus.by.ISC.effect.sizes <- tibble(
  Compartment = desulfosporosinus.by.ISC.compartment.eta.squared,
  Smooth_by_Root = desulfosporosinus.by.ISC.root.eta.squared,
  Smooth_by_Soil = desulfosporosinus.by.ISC.soil.eta.squared
)
```

## Desulfosporosinus Effect Size Summary

Table 38: Summary of effect sizes (partial eta-squared) for the Desulfosporosinus abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.42970	0	0.01539
HII	0.45085	0	0.05075
ISC	0.51041	0	0.21359

## Desulfocapsa

### Distance

```
## Get model residuals
desulfocapsa.by.distance.residual.df <- df.residual(
  desulfocapsa.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfocapsa.by.distance.compartment.eta.squared <- F_to_eta2(
  14.2, 1, desulfocapsa.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
desulfocapsa.by.distance.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfocapsa.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
desulfocapsa.by.distance.soil.eta.squared <- F_to_eta2(
  0.816, 0.920, desulfocapsa.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfocapsa.by.distance.effect.sizes <- tibble(
  Compartment = desulfocapsa.by.distance.compartment.eta.squared,
  Smooth_by_Root = desulfocapsa.by.distance.root.eta.squared,
  Smooth_by_Soil = desulfocapsa.by.distance.soil.eta.squared
)
```



## Human Influence Index

```
## Get model residuals
desulfocapsa.by.HII.residual.df <- df.residual(
  desulfocapsa.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfocapsa.by.HII.compartment.eta.squared <- F_to_eta2(
  14.2, 1, desulfocapsa.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
desulfocapsa.by.HII.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfocapsa.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
desulfocapsa.by.HII.soil.eta.squared <- F_to_eta2(
  0.823, 0.881, desulfocapsa.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfocapsa.by.HII.effect.sizes <- tibble(
  Compartment = desulfocapsa.by.HII.compartment.eta.squared,
  Smooth_by_Root = desulfocapsa.by.HII.root.eta.squared,
  Smooth_by_Soil = desulfocapsa.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
desulfocapsa.by.ISC.residual.df <- df.residual(
  desulfocapsa.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
desulfocapsa.by.ISC.compartment.eta.squared <- F_to_eta2(
  14.1, 1, desulfocapsa.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
desulfocapsa.by.ISC.root.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfocapsa.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
desulfocapsa.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, desulfocapsa.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
desulfocapsa.by.ISC.effect.sizes <- tibble(
  Compartment = desulfocapsa.by.ISC.compartment.eta.squared,
  Smooth_by_Root = desulfocapsa.by.ISC.root.eta.squared,
  Smooth_by_Soil = desulfocapsa.by.ISC.soil.eta.squared
)
```

## Desulfocapsa Effect Size Summary

Table 39: Summary of effect sizes (partial eta-squared) for the Desulfocapsa abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.17471	0	0.01107
HII	0.17462	0	0.01069
ISC	0.17572	0	0.00000

## Phyllobacterium

### Distance

```
## Get model residuals
phyllobacterium.by.distance.residual.df <- df.residual(
  phyllobacterium.by.distance.GAM
)

## Calculate effect sizes
# Compartment (parametric)
phyllobacterium.by.distance.compartment.eta.squared <- F_to_eta2(
  38.9, 1, phyllobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by root
phyllobacterium.by.distance.root.eta.squared <- F_to_eta2(
  0.056, 0.339, phyllobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of distance by soil
phyllobacterium.by.distance.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, phyllobacterium.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
phyllobacterium.by.distance.effect.sizes <- tibble(
  Compartment = phyllobacterium.by.distance.compartment.eta.squared,
  Smooth_by_Root = phyllobacterium.by.distance.root.eta.squared,
  Smooth_by_Soil = phyllobacterium.by.distance.soil.eta.squared
)
```

## Human Influence Index

```
## Get model residuals
phyllobacterium.by.HII.residual.df <- df.residual(
  phyllobacterium.by.HII.GAM
)

## Calculate effect sizes
# Compartment (parametric)
phyllobacterium.by.HII.compartment.eta.squared <- F_to_eta2(
  41.6, 1, phyllobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by root
phyllobacterium.by.HII.root.eta.squared <- F_to_eta2(
  0.574, 0.838, phyllobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of HII by soil
phyllobacterium.by.HII.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, phyllobacterium.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
phyllobacterium.by.HII.effect.sizes <- tibble(
  Compartment = phyllobacterium.by.HII.compartment.eta.squared,
  Smooth_by_Root = phyllobacterium.by.HII.root.eta.squared,
  Smooth_by_Soil = phyllobacterium.by.HII.soil.eta.squared
)
```

## Mean ISC

```
## Get model residuals
phyllobacterium.by.ISC.residual.df <- df.residual(
  phyllobacterium.by.ISC.GAM
)

## Calculate effect sizes
# Compartment (parametric)
phyllobacterium.by.ISC.compartment.eta.squared <- F_to_eta2(
  41.2, 1, phyllobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by root
phyllobacterium.by.ISC.root.eta.squared <- F_to_eta2(
  0.487, 0.834, phyllobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# Smooth of ISC by soil
phyllobacterium.by.ISC.soil.eta.squared <- F_to_eta2(
  0.00001, 0.00001, phyllobacterium.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
phyllobacterium.by.ISC.effect.sizes <- tibble(
  Compartment = phyllobacterium.by.ISC.compartment.eta.squared,
  Smooth_by_Root = phyllobacterium.by.ISC.root.eta.squared,
  Smooth_by_Soil = phyllobacterium.by.ISC.soil.eta.squared
)
```

## Phyllobacterium Effect Size Summary

Table 40: Summary of effect sizes (partial eta-squared) for the Phyllobacterium abundance GAMs.

Urbanization_Metric	Compartment	Smooth_by_Root	Smooth_by_Soil
Distance	0.36505	0.00028	0
HII	0.38249	0.00711	0
ISC	0.38019	0.00601	0

# Carbon & Nitrogen Effect Sizes

## Soil Total Carbon

```
## Get model residuals
# Distance
soil.total.C.by.distance.residual.df <- df.residual(
  soil.total.C.by.distance.GAM
)
# HII
soil.total.C.by.HII.residual.df <- df.residual(
  soil.total.C.by.HII.GAM
)
# ISC
soil.total.C.by.ISC.residual.df <- df.residual(
  soil.total.C.by.ISC.GAM
)

## Calculate effect sizes
# Distance
soil.total.C.by.distance.eta.squared <- F_to_eta2(
  1.604, 2.518, soil.total.C.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
soil.total.C.by.HII.eta.squared <- F_to_eta2(
  0.679, 0.859, soil.total.C.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
soil.total.C.by.ISC.eta.squared <- F_to_eta2(
  1.867, 2.452, soil.total.C.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
soil.total.C.effect.sizes <- tibble(
  Distance = soil.total.C.by.distance.eta.squared,
  HII = soil.total.C.by.HII.eta.squared,
  ISC = soil.total.C.by.ISC.eta.squared
)
```

Table 41: Summary of effect sizes (partial eta-squared) for the soil total C GAMs.

Distance	HII	ISC
0.1137	0.0173	0.12672



## Soil Delta 13C

```
## Get model residuals
# Distance
soil.delta.13C.by.distance.residual.df <- df.residual(
  soil.delta.13C.by.distance.GAM
)
# HII
soil.delta.13C.by.HII.residual.df <- df.residual(
  soil.delta.13C.by.HII.GAM
)
# ISC
soil.delta.13C.by.ISC.residual.df <- df.residual(
  soil.delta.13C.by.ISC.GAM
)

## Calculate effect sizes
# Distance
soil.delta.13C.by.distance.eta.squared <- F_to_eta2(
  2.141, 1.039, soil.delta.13C.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
soil.delta.13C.by.HII.eta.squared <- F_to_eta2(
  1.039, 0.904, soil.delta.13C.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
soil.delta.13C.by.ISC.eta.squared <- F_to_eta2(
  0.954, 0.939, soil.delta.13C.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
soil.delta.13C.effect.sizes <- tibble(
  Distance = soil.delta.13C.by.distance.eta.squared,
  HII = soil.delta.13C.by.HII.eta.squared,
  ISC = soil.delta.13C.by.ISC.eta.squared
)
```

Table 42: Summary of effect sizes (partial eta-squared) for the soil delta 13C GAMs.

Distance	HII	ISC
0.06322	0.0276	0.02638

## Leaf Total Carbon

```
## Get model residuals
# Distance
leaf.total.C.by.distance.residual.df <- df.residual(
  leaf.total.C.by.distance.GAM
)
# HII
leaf.total.C.by.HII.residual.df <- df.residual(
  leaf.total.C.by.HII.GAM
)
# ISC
leaf.total.C.by.ISC.residual.df <- df.residual(
  leaf.total.C.by.ISC.GAM
)

## Calculate effect sizes
# Distance
leaf.total.C.by.distance.eta.squared <- F_to_eta2(
  0.00001, 0.00001, leaf.total.C.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
leaf.total.C.by.HII.eta.squared <- F_to_eta2(
  0.00001, 0.00001, leaf.total.C.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
leaf.total.C.by.ISC.eta.squared <- F_to_eta2(
  0.872, 1.841, leaf.total.C.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
leaf.total.C.effect.sizes <- tibble(
  Distance = leaf.total.C.by.distance.eta.squared,
  HII = leaf.total.C.by.HII.eta.squared,
  ISC = leaf.total.C.by.ISC.eta.squared
)
```

Table 43: Summary of effect sizes (partial eta-squared) for the leaf total C GAMs.

Distance	HII	ISC
0	0	0.04755

## Leaf Delta 13C

```
## Get model residuals
# Distance
leaf.delta.13C.by.distance.residual.df <- df.residual(
  leaf.delta.13C.by.distance.GAM
)
# HII
leaf.delta.13C.by.HII.residual.df <- df.residual(
  leaf.delta.13C.by.HII.GAM
)
# ISC
leaf.delta.13C.by.ISC.residual.df <- df.residual(
  leaf.delta.13C.by.ISC.GAM
)

## Calculate effect sizes
# Distance
leaf.delta.13C.by.distance.eta.squared <- F_to_eta2(
  0.279, 0.730, leaf.delta.13C.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
leaf.delta.13C.by.HII.eta.squared <- F_to_eta2(
  0.043, 0.278, leaf.delta.13C.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
leaf.delta.13C.by.ISC.eta.squared <- F_to_eta2(
  0.087, 0.442, leaf.delta.13C.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
leaf.delta.13C.effect.sizes <- tibble(
  Distance = leaf.delta.13C.by.distance.eta.squared,
  HII = leaf.delta.13C.by.HII.eta.squared,
  ISC = leaf.delta.13C.by.ISC.eta.squared
)
```

Table 44: Summary of effect sizes (partial eta-squared) for the leaf delta 13C GAMs.

Distance	HII	ISC
0.00608	0.00035	0.00114

## Soil Total Nitrogen

```
## Get model residuals
# Distance
soil.total.N.by.distance.residual.df <- df.residual(
  soil.total.N.by.distance.GAM
)
# HII
soil.total.N.by.HII.residual.df <- df.residual(
  soil.total.N.by.HII.GAM
)
# ISC
soil.total.N.by.ISC.residual.df <- df.residual(
  soil.total.N.by.ISC.GAM
)

## Calculate effect sizes
# Distance
soil.total.N.by.distance.eta.squared <- F_to_eta2(
  0.546, 0.851, soil.total.N.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
soil.total.N.by.HII.eta.squared <- F_to_eta2(
  0.024, 0.179, soil.total.N.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
soil.total.N.by.ISC.eta.squared <- F_to_eta2(
  0.141, 0.563, soil.total.N.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
soil.total.N.effect.sizes <- tibble(
  Distance = soil.total.N.by.distance.eta.squared,
  HII = soil.total.N.by.HII.eta.squared,
  ISC = soil.total.N.by.ISC.eta.squared
)
```

Table 45: Summary of effect sizes (partial eta-squared) for the soil total N GAMs.

Distance	HII	ISC
0.01382	0.00013	0.00237

## Soil Delta 15N

```
## Get model residuals
# Distance
soil.delta.15N.by.distance.residual.df <- df.residual(
  soil.delta.15N.by.distance.GAM
)
# HII
soil.delta.15N.by.HII.residual.df <- df.residual(
  soil.delta.15N.by.HII.GAM
)
# ISC
soil.delta.15N.by.ISC.residual.df <- df.residual(
  soil.delta.15N.by.ISC.GAM
)

## Calculate effect sizes
# Distance
soil.delta.15N.by.distance.eta.squared <- F_to_eta2(
  1.306, 0.968, soil.delta.15N.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
soil.delta.15N.by.HII.eta.squared <- F_to_eta2(
  1.521, 0.932, soil.delta.15N.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
soil.delta.15N.by.ISC.eta.squared <- F_to_eta2(
  1.192, 0.950, soil.delta.15N.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
soil.delta.15N.effect.sizes <- tibble(
  Distance = soil.delta.15N.by.distance.eta.squared,
  HII = soil.delta.15N.by.HII.eta.squared,
  ISC = soil.delta.15N.by.ISC.eta.squared
)
```

Table 46: Summary of effect sizes (partial eta-squared) for the soil delta 15N GAMs.

Distance	HII	ISC
0.03686	0.04111	0.03313

## Leaf Total Nitrogen

```
## Get model residuals
# Distance
leaf.total.N.by.distance.residual.df <- df.residual(
  leaf.total.N.by.distance.GAM
)
# HII
leaf.total.N.by.HII.residual.df <- df.residual(
  leaf.total.N.by.HII.GAM
)
# ISC
leaf.total.N.by.ISC.residual.df <- df.residual(
  leaf.total.N.by.ISC.GAM
)

## Calculate effect sizes
# Distance
leaf.total.N.by.distance.eta.squared <- F_to_eta2(
  3.065, 3.070, leaf.total.N.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
leaf.total.N.by.HII.eta.squared <- F_to_eta2(
  0.029, 0.207, leaf.total.N.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
leaf.total.N.by.ISC.eta.squared <- F_to_eta2(
  1.364, 1.916, leaf.total.N.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
leaf.total.N.effect.sizes <- tibble(
  Distance = leaf.total.N.by.distance.eta.squared,
  HII = leaf.total.N.by.HII.eta.squared,
  ISC = leaf.total.N.by.ISC.eta.squared
)
```

Table 47: Summary of effect sizes (partial eta-squared) for the leaf total N GAMs.

Distance	HII	ISC
0.23326	0.00018	0.07532

## Leaf Delta 15N

```
## Get model residuals
# Distance
leaf.delta.15N.by.distance.residual.df <- df.residual(
  leaf.delta.15N.by.distance.GAM
)
# HII
leaf.delta.15N.by.HII.residual.df <- df.residual(
  leaf.delta.15N.by.HII.GAM
)
# ISC
leaf.delta.15N.by.ISC.residual.df <- df.residual(
  leaf.delta.15N.by.ISC.GAM
)

## Calculate effect sizes
# Distance
leaf.delta.15N.by.distance.eta.squared <- F_to_eta2(
  0.090, 0.450, leaf.delta.15N.by.distance.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# HII
leaf.delta.15N.by.HII.eta.squared <- F_to_eta2(
  0.028, 0.200, leaf.delta.15N.by.HII.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()
# ISC
leaf.delta.15N.by.ISC.eta.squared <- F_to_eta2(
  0.127, 0.537, leaf.delta.15N.by.ISC.residual.df
) %>%
  select(Eta2_partial) %>%
  as.numeric()

## Set tibble of effect sizes
leaf.delta.15N.effect.sizes <- tibble(
  Distance = leaf.delta.15N.by.distance.eta.squared,
  HII = leaf.delta.15N.by.HII.eta.squared,
  ISC = leaf.delta.15N.by.ISC.eta.squared
)
```

Table 48: Summary of effect sizes (partial eta-squared) for the leaf delta 15N GAMs.

Distance	HII	ISC
0.00121	0.00017	0.00203

## R Session Information

Table 49: Packages required for data management and analysis.

Package	Loaded Version	Date
bayestestR	0.13.2	2024-02-12
correlation	0.8.4	2023-04-06
datawizard	0.10.0	2024-03-26
dplyr	1.1.4	2023-11-17
easystats	0.7.1	2024-03-28
effectsize	0.8.7	2024-04-01
forcats	1.0.0	2023-01-29
ggplot2	3.5.1	2024-04-23
insight	0.19.10	2024-03-22
kableExtra	1.4.0	2024-01-24
knitr	1.46	2024-04-06
lubridate	1.9.3	2023-09-27
mgcv	1.9-1	2023-12-21
modelbased	0.8.7	2024-02-15
nlme	3.1-164	2023-11-27
parameters	0.21.6	2024-03-18
performance	0.11.0	2024-03-22
purrr	1.0.2	2023-08-10
readr	2.1.5	2024-01-10
report	0.5.8	2023-12-07
see	0.8.4	2024-04-29
stringr	1.5.1	2023-11-14
tibble	3.2.1	2023-03-20
tidyr	1.3.1	2024-01-24
tidyverse	2.0.0	2023-02-22